

Run on:	March 17, 2003, 08:49:19	Search time 159 seconds	7	2055	50.7	695	27	US-60-360-039-9656	Sequence 9965, AP
Om protein - protein search, using sw model		(without alignments)	8	2037.5	50.0	710	27	US-60-360-039-15849	Sequence 15849, AP
Copyright (c) 1993 - 2003 Compugen Ltd.		3154.732 Million cell updates/sec	9	2018.5	49.8	711	27	US-60-360-039-15479	Sequence 15479, AP
Title: Perfect score: 4055	US-10-010-227-3	Sequence 1 MPGABSTFQTLYDKVLQAHV.....KAVPVPTTNRGEKKKEPLEW 778	10	1995	49.2	752	27	US-60-360-039-9413	Sequence 9413, AP
Scoring table: BLASTM62		Gapop 10.0 , Gapext 0.5	11	1978	48.8	755	27	US-60-360-039-7883	Sequence 17883, AP
Searched: 4569144 seqs, 64473110 residues			12	1963.5	48.4	749	27	US-60-360-039-9308	Sequence 9308, AP
Minimum DB seq length: 0			13	1955.5	48.2	681	27	US-60-360-039-8616	Sequence 8616, AP
Maximum DB seq length: 200000000			14	1891	46.5	740	27	US-60-360-039-7437	Sequence 7437, AP
Post-processing: Minimum Match 0%			15	1881	46.4	729	27	US-60-360-039-4678	Sequence 4677, AP
Database : Pending Patents AA Main:*			16	1861	45.9	686	27	US-60-360-039-7055	Sequence 7055, AP
1: /cgn2_6/ptodata/2/paa/PCFTUS COMB.pep:*			17	1857	45.8	688	27	US-60-360-039-4299	Sequence 4299, AP
2: /cgn2_6/ptodata/2/paa/US06_Comb.pep:*			18	1711.5	42.2	672	27	US-60-360-039-9059	Sequence 9059, AP
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*			19	1697.5	41.9	676	27	US-60-360-039-19463	Sequence 10463, AP
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*			20	1682.5	41.5	646	27	US-60-360-039-16643	Sequence 16643, AP
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*			21	1670.5	41.2	679	27	US-60-360-039-14041	Sequence 14041, AP
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*			22	1665.5	41.1	644	1	PCT-US02-03987-5720	Sequence 5720, AP
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*			23	1665.5	41.1	644	22	US-09-815-942-5730	Sequence 5730, AP
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*			24	1665.5	41.1	644	24	US-10-072-851-5730	Sequence 5730, AP
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*			25	1665.5	41.1	644	27	US-60-242-578-1009	Sequence 1009, AP
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*			26	1665.5	41.1	644	27	US-253-525-25-253	Sequence 2353, AP
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*			27	1666.5	41.1	644	27	US-60-269-008-4336	Sequence 3311, AP
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*			28	1666.5	40.8	517	18	US-09-417-507-37934	Sequence 4336, AP
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*			29	1595.5	39.3	668	27	US-60-360-039-8819	Sequence 37934, AP
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*			30	1595.5	39.3	668	27	US-60-360-039-10002	Sequence 8819, AP
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*			31	1586	39.1	469	27	US-60-360-039-1582	Sequence 15002, AP
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*			32	1555	38.3	469	24	US-09-227-10081	Sequence 10081, AP
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*			33	1548.5	38.2	469	21	US-09-791-537-20546	Sequence 20646, AP
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*			34	1545.5	38.1	469	21	US-09-791-537-33097	Sequence 33097, AP
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*			35	1529.5	37.7	471	27	US-09-360-039-17906	Sequence 19706, AP
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*			36	1520.5	37.5	526	17	US-09-328-352-8024	Sequence 8024, AP
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep:*			37	1508	37.2	672	27	US-60-360-039-7323	Sequence 7323, AP
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*			38	1507.5	37.2	474	1	PCT-US02-03987-5127	Sequence 5127, AP
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*			39	1507.5	37.2	474	22	US-09-815-212-5127	Sequence 5127, AP
24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*			40	1507.5	37.2	474	24	US-10-072-851-5127	Sequence 5127, AP
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*			41	1507.5	37.2	474	27	US-60-265-2683	Sequence 2683, AP
26: /cgn2_6/ptodata/2/paa/US102_COMB.pep:*			42	1507.5	37.2	474	27	US-60-257-931-3511	Sequence 3511, AP
27: /cgn2_6/ptodata/2/paa/US103_COMB.pep:*			43	1507.5	37.2	474	27	US-60-269-308-4533	Sequence 4533, AP
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			44	1507.5	37.2	480	16	US-09-791-537-28666	Sequence 28668, AP
Result No.	Score	Query Match Length DB ID	45	1494	36.8	670	27	US-60-360-039-4565	Sequence 4565, AP
1	4055	100.0	778	24	US-10-010-227-3	Sequence 10021, AP			
2	3397	83.8	840	27	US-60-360-039-3233	Sequence 10021, AP			
3	2456.5	60.6	779	27	US-60-360-039-21952	Sequence 10021, AP			
4	2451.5	60.5	794	25	US-10-179-131-8614	Sequence 10021, AP			
5	2076	51.2	644	21	US-09-791-537-121852	Sequence 10021, AP			
6	2068.5	51.0	875	27	US-60-360-039-7864	Sequence 10021, AP			
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7	2055	50.7	695	27	US-60-360-039-9656	Sequence 9965, AP			
8	2037.5	50.0	710	27	US-60-360-039-15849	Sequence 15849, AP			
9	2018.5	49.8	711	27	US-60-360-039-15479	Sequence 15479, AP			
10	1995	49.2	752	27	US-60-360-039-9413	Sequence 9413, AP			
11	1978	48.8	755	27	US-60-360-039-7883	Sequence 17883, AP			
12	1963.5	48.4	749	27	US-60-360-039-9308	Sequence 9308, AP			
13	1955.5	48.2	681	27	US-60-360-039-8616	Sequence 10463, AP			
14	1891	46.5	740	27	US-60-360-039-7437	Sequence 16643, AP			
15	1881	46.4	729	27	US-60-360-039-4678	Sequence 14041, AP			
16	1861	45.9	686	27	US-60-360-039-7055	Sequence 20646, AP			
17	1857	45.8	688	27	US-60-360-039-4299	Sequence 4677, AP			
18	1711.5	42.2	672	27	US-60-360-039-9059	Sequence 5720, AP			
19	1697.5	41.9	676	27	US-60-360-039-19463	Sequence 5730, AP			
20	1682.5	41.5	646	27	US-60-360-039-16643	Sequence 5730, AP			
21	1670.5	41.2	679	27	US-60-360-039-14041	Sequence 5730, AP			
22	1665.5	41.1	644	1	PCT-US02-03987-5720	Sequence 5720, AP			
23	1665.5	41.1	644	22	US-10-072-851-5730	Sequence 5730, AP			
24	1665.5	41.1	644	24	US-10-072-851-51021	Sequence 51021, AP			
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28	1666.5	41.1	644	27	US-60-269-008-4336	Sequence 3311, AP			
29	1666.5	40.8	517	18	US-09-417-507-37934	Sequence 4336, AP			
30	1595.5	39.3	668	27	US-60-360-039-8819	Sequence 37934, AP			
31	1586	39.1	469	27	US-60-360-039-10002	Sequence 15002, AP			
32	1555	38.3	469	21	US-09-791-537-20546	Sequence 20646, AP			
33	1548.5	38.2	469	21	US-09-791-537-33097	Sequence 33097, AP			
34	1545.5	38.1	469	27	US-09-360-039-17906	Sequence 19706, AP			
35	1529.5	37.7	471	27	US-09-328-352-8024	Sequence 8024, AP			
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37	1508	37.2	672	27	US-60-360-039-7323	Sequence 7323, AP			
38	1507.5	37.2	474	1	PCT-US02-03987-5127	Sequence 5127, AP			
39	1507.5	37.2	474	22	US-09-815-212-5127	Sequence 5127, AP			
40	1507.5	37.2	474	24	US-10-072-851-5127	Sequence 5127, AP			
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42	1507.5	37.2	474	27	US-60-257-931-3511	Sequence 3511, AP			
43	1507.5	37.2	474	27	US-60-269-308-4533	Sequence 4533, AP			
44	1507.5	37.2	480	16	US-09-791-537-28666	Sequence 28668, AP			
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47	1483.5	36.6	466	18	US-09-489-091-537-1522	Sequence 12322, AP			
48	1481.5	36.5	466	21	US-09-791-537-84058	Sequence 84058, AP			
49	1479.5	36.5	466	1	PCT-US02-03987-10021	Sequence 10021, AP			
50	1479.5	36.5	466	22	US-09-815-242-11164	Sequence 11164, AP			
51	1479.5	36.5	466	22	US-09-815-242-1021	Sequence 11164, AP			
52	1479.5	36.5	466	22	US-09-815-242-1021	Sequence 11164, AP			
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62	1449.5	35.6	466	25	US-09-791-537-82623	Sequence 82623, AP			
63	1439.5	35.5	487	19	US-09-791-537-84859	Sequence 84859, AP			
64	1439.5	35.5	485	21	US-09-791-537-84859	Sequence 84859, AP			
65	1413	34.8	475	21	US-09-791-537-74515	Sequence 82611, AP			
66	1399.5	34.4	472	21	US-09-791-537-74515	Sequence 82611, AP			
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68	1395.5	34.2	476	21	US-09-791-537-74515	Sequence 82611, AP			
69	1383.5	34.2	473	21	US-09-791-537-74515	Sequence 82611, AP			
70	1383.5	34.1	471	21	US-09-791-537-74515	Sequence 82611, AP			
71	1354.5	33.4	466	21	US-09-791-537-74515	Sequence 82611, AP			
72	1354.5	33.4	469	21	US-09-791-537-74515	Sequence 82611, AP			
73	1354.5	33.4	476	21	US-09-791-537-74515	Sequence 82611, AP			
74	1347.5	33.2	481	21	US-09-791-537-74515	Sequence 82611, AP			
75	1330	32.8	471	21	US-09-791-537-74515	Sequence 82611, AP			
76	1330	32.8	553	20	US-09-606-740-266	Sequence 82611, AP			
77	1321.5	32.6							

RESULT 1
US-10-010-227-3
Sequence 3, Application US/10010227
GENERAL INFORMATION:
APPLICANT: Hauer, Lisbeth
APPLICANT: Adachi, Kiichi
APPLICANT: Dezaan, Todd M
APPLICANT: Lo, Sze Chung C
APPLICANT: Montenegro-Chamorro, Maria V
APPLICANT: Frank, Sheryl A
APPLICANT: Darveaux, Blaise A
APPLICANT: Mahanty, Sanjoy K
APPLICANT: Heiniger, Ryan W
APPLICANT: Skalchunes, Amy R
APPLICANT: Pan, Ruqin
APPLICANT: Tarpey, Rex
APPLICANT: Shuster, Jeffrey R
APPLICANT: Tanzer, Matthew M
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF INHIBITORS OF 3-ISOPROPYLALATE
TITLE OF INVENTION: DEHYDRATASE AS ANTIOTICS
FILE REFERENCE: 2131US
CURRENT APPLICATION NUMBER: US/10/010 / 227
CURRENT FILING DATE: 2001-12-06
SOFTWARE: Patent version 3.1
SEQ ID NO 3
LENGTH: 778
TYPE: PRT
ORGANISM: Magnaporthe grisea

US-10-010-227-3

Query Match 100.0% ; Score 4055 ; DB 24 ; Length 778 ;
Best Local Similarity 100.0% ; Pred. No. 0 ;
Matches 778 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

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Qy 61 DCTLATTDHNVPTTSRALKDIAFSIKEDDSRTRQCVTLEENVKEFGVYTFGLSDKRGIV 120
Db 61 DCTLATTDHNVPTTSRALKDIAFSIKEDDSRTRQCVTLEENVKEFGVYTFGLSDKRGIV 120

Qy 121 HVIGPQQGFTLPGTTVUCGDSHTSSTGAFGALAFGCTSEVHVLATQCLTRKSKNMR 180
Db 121 HVIGPQQGFTLPGTTVUCGDSHTSSTGAFGALAFGCTSEVHVLATQCLTRKSKNMR 180

Sequence 55954, A
Sequence 10096, A
Sequence 9086, A
Sequence 12156, A
Sequence 12928, A
Sequence 5398, A
Sequence 6093, A
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Sequence 10069, A
Sequence 4868, A
Sequence 15039, A
Sequence 19849, A
Sequence 18911, A
Sequence 81237, A
Sequence 18414, A
Sequence 131423, A
Sequence 37932, A
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Qy 241 RAGMYAPDEITEFYLKGRPLAKYDSDPGAKYDIDYFIDADIVP 300
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Qy 301 TLTWGSPEDVVPITCVPDDETFATEAKADGRMLQYMGKAGTGMEDIPVDKVFGS 360
Db 301 TLTWGSPEDVVPITCVPDDETFATEAKADGRMLQYMGKAGTGMEDIPVDKVFGS 360
Qy 361 CTNSRILEDRAAAAYVKGKKAAPNTSAMVPGSGLVYKTOAEEGDKIFEEAGFVRE 420
Db 361 CTNSRILEDRAAAAYVKGKKAAPNTSAMVPGSGLVYKTOAEEGDKIFEEAGFVRE 420
Qy 421 GCSMCIGMNPDLIAQPERCASTSNRNFEGROGAGGFTHLSPVMAAAGIVKLADYRKL 480
Db 421 GCSMCIGMNPDLIAQPERCASTSNRNFEGROGAGGFTHLSPVMAAAGIVKLADYRKL 480
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Db 481 TDYKASPHIAYQSKTIVKPHDVERINQDAHEKDITADIPIPDDNGHTNTSASVGTASGL 540
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Qy 661 IKDQDQIEAAEAFAGKEEVLDLNQLNKATGETCTFVEEVFKHCLYGLDDGILT 720
Db 661 IKDQDQIEAAEAFAGKEEVLDLNQLNKATGETCTFVEEVFKHCLYGLDDGILT 720
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Db 721 MQMEDRIAEFEAKMOTRETPMLDGTSYLRKGQGGKLAAKAVPVPTNRGEEKEKPELW 778
RESULT 2
US-6-360-039-3233
; Sequence 3233, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S
; APPLICANT: Hinkle, Gregory J
; APPLICANT: Slater, Steven C
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; CURRENT APPLICATION NUMBER: US/60/360, 039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3233
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE: unsure
; LOCATION: (1) .. (840)
; OTHER INFORMATION: unsure at all xaa locations
US-6-360-039-3233

Query Match 83.8% ; Score 3397 ; DB 27 ; Length 840 ;
Best Local Similarity 77.8% ; Pred. No. 0 ;
Matches 655 ; Conservative 53 ; Mismatches 60 ; Indels 74 ; Gaps 5 ;
Qy 9 QTLYDKVLOAHVYDEKLDSRTRQCVTLEENVKEFGVYTFGLSDKRGIV 120
Db 1 RTLYDKVFOQAHVYDEKLDSRTRQCVTLEENVKEFGVYTFGLSDKRGIV 120
44

; SEQ ID NO 21952
; LENGTH: 779
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*
; US-6-360-039-21952

Query Match: 60.6%; Score 2456.5; DB 27; Length 779;
Best Local Similarity: 63.1%; Pred. No. 5.3e-236; Gaps 10;
Matches 486; Conservative 93; Mismatches 152; Indels 39; Gaps 10;

QY 45 -QAFEGIRNAGRKVRPDPCTIATDH----- 69
Db 61 1QAFEGIRNAGRKVRPDPCTIATDHSSMLPLFFYFHMAMAFAFSRPRXPLAPSOLCG 120

QY 70 -----NVPITSRKALKDIASTFIKEEDSRRTQCVTLEENVKERVGTVTFLGSLDKRQGI 119
Db 121 TASXPTRCRMVPTSRKALKDIASTFIKEEDSRRTQCVTLEENVKERVGTVTFLGSLDKRQGI 180

QY 120 VHVIQEPEQFELPQGTVWCGSHTSRTHGAFALAFGIGTSEVEHVLATQCVTLEENVKERVGTVTFLGSLDKRQGI 179
Db 181 VHVIQEPEQFELPQGTVWCGSHTSRTHGAFALAFGIGTSEVEHVLATQCVTLEENVKERVGTVTFLGSLDKRQGI 240

QY 240 ARAGMVADETFEYIKGRPLAPKVDPSPEWIKATQCVTLEENVKERVGTVTFLGSLDKRQGI 299
Db 301 ARAGMVADETFEYIKGRPLAPKVDPSPEWIKATQCVTLEENVKERVGTVTFLGSLDKRQGI 360

QY 300 PTLTWGSPEWDVPTGWPDPETATEAKADGRMLQYMLKAGTPMEDIPTVDFKFIG 359
Db 361 PTVTWGSPEWDVPTGWPDPETATEAKADGRMLQYMLKAGTPMEDIPTVDFKFIG 420

QY 360 SCTNSRILEDRAAVVUGRKCKAPNVSAMVPGSGLVKTQAEEGLKDIPBEGFRE 419
Db 421 SCTNSRILEDRAAVVUGRKCKAPNVSAMVPGSGLVKTQAEEGLKDIPBEGFRE 480

QY 420 AGCSMCILGMNPDLAFOERCASTSNRNFEGRCAGGRTHLMSPVMAAAGIYVKLADWRK 479
Db 481 AGCSMCILGMNPDLAFOERCASTSNRNFEGRCAGGRTHLMSPVMAAAGIYVKLADWRK 540

QY 480 LTDYKASPHIAVY--OKSTVTKPHVBERINDAHEKIDTADIPEDNNGPHTNTASVGT 536
Db 541 LTDYKASPHIAVY--OKSTVTKPHVBERINDAHEKIDTADIPEDNNGPHTNTASVGT 598

QY 537 SAGLPKFTILKGIAAPLEKANVDTAIPKQFLTIKETGIGLNLQYMLKAGTPMEDIPTVDFKFIG 596
Db 599 SAGLPKFTILKGIAAPLEKANVDTAIPKQFLTIKETGIGLNLQYMLKAGTPMEDIPTVDFKFIG 658

QY 597 FVUNKEPKRKAStLVCAGANFGCSSLREHAPWALNDFGIRSVAAPSADIFFNNSFGKM 656
Db 659 FVUNKEPKRKAStLVCAGANFGCSSLREHAPWALNDFGIRSVAAPSADIFFNNSFGKM 718

QY 657 LIPIKQOQIAIAEERAKGKEIEVDLNPQLKNTATCETCIFEVERFRKICLVLNGDD 716
Db 719 LPIAKDQAKALEVHAEAGRTEIDLPNQLKDADNTLCFEEVERFRKICLVLNGDD 778

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Db 779 IGLTMQMDKIAFEAKMTRTFLDGTGKLRKGQGSKLAAGAVPVTTNGEEKKEPL 838

QY 777 EW 778
Db 839 EW 840

RESULT 3
US-60-030-039-21952
; Sequence 21952, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slatner, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10 (52052)A
; CURRENT APPLICATION NUMBER: US/60/360, 039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 473/4

RESULT 4
US-10-179-131-8614
; Sequence 8614, Application US/10179131
; GENERAL INFORMATION:
; APPLICANT: HARE, ROBERTA S.
; APPLICANT: SHAW, KAREN J.
; APPLICANT: SHIMER JR., GEORGE H.
; APPLICANT: KESSLER, MARCO
; APPLICANT: NOLLING, JORK
; APPLICANT: ZENG, QIANDONG

APPLICANT: Hinkle, Gregory J.
C.
ATTORNEY: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (55052) A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO: 7864
LENGTH: 875
TYPE: PRT
ORGANISM: Rhodobacter sphaeroides
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(875)
OTHER INFORMATION: unsure at all xaa locations
S-60-360-039-7864

RESULT 7
US-60-3360-039-9965
; Sequence 9965, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianteng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; .

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RESULT 7
US-60-360-039-9965
; Sequence 9965, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianteng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: B-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9965
; LENGTH: 695
; TYPE: PRT
; ORGANISM: magnetite-containing magnetic coccus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(695)
; OTHER INFORMATION: unsure at all Xaa locations
; US-60-360-039-9965

Query Match          50.7%;  Score 2055;  DB 27;  Length 695;
Best Local Similarity 56.8%;  Pred. No. 8..9e-196;  Matches 422;  Conservative 89;  Mismatches 168;  Indels 64;  Gaps 11;
QY  9  QTYLDKVLQAHVDEKLDGTVLIVIDRHLVHRTVSPQAEGRLRNAGKVRKRRDCTLATT 68
Db  6  QTLFEKTKWNAHLIRTDGTSILVYDHLVHRTVSPQAEGRLAGKVRHBEATPAVDP 65
QY  69  HNVPPTSRKALDIASTPKEDDSRTCTVLEENVKEGVTVGLSDKRGIVHVGVBQ 128
Db  66  HNVPPT-----KDLAGGIKDPVSKLQVDTLASNCQAFGITEFVGVDLQRQGVHVMAPBQG 119
QY  129  FILPGTIVVUCGHSHTSITGAGFALAFGIGTSEVHVLATOCILTRSKKMRQVDGELAP 188
Db  120  ISLPGFTMWCGDSHTATHGAGFALAFGIGTSEVHVLATOTLMOKKPKTMLIQVEGELP 179
QY  189  GYSSKDVTWHAITGIGTAGTGAVIERCGSVTRSLSBARMSITCNMSIEGGARAGMVPD 248
Db  180  GSTAKDILLYIGNIGTAGGIGVLEFGGSAIQALSMERGMIVCNMIAEAGARAGMVAW 239
QY  249  EITFEYUKGRPLAKYDSDPEHMKATQWKNLQSDPGAKYDDVFDKDIVPTLWGMSP 308
Db  240  EKTAIYVQGRPYAPKGKA- -WKAQAOQMTLKSDEGAAPFDVWLTDAINTIAPOVWTGSP 297
QY  309  EDWVPTGVPDPETATEKAGDGRMLQYQMGKLAGKTPMEDIYDVKUFIGSCNSRIED 368
Db  298  ELVAPUDGVCPVPTDEENGVKRGAMEKALAYWGLQACTPMTLEAVDKVFFIGSCTNSRIED 357
QY  369  LRAAAAVVKGKRPKAAPNTKSAMTYPGSGLVIKTOBEEGLDKTREBAGEFWREACCSMCIGM 428
Db  358  LRAAAAVAVGKKAASIKALAVPGTGLVKOOROEGLDKIFMEAGFEEWREFOCSMCLAM 417
QY  429  NPDILAQERCASTSNENFEGGAGGERTHMSPWMAAAGIVGKLAQDVRKLTJDYKASPH 488
Db  418  NNDVLEGERCCASTSNRNPFGROKGDSRTHLVSPAMAAAIAGHFVDIR--NGKAS-G 473
Db  489  IAYOKSTVTKPHVDERINQDAHEKDIIAD-PDNNGPHINTSASVGTAGLKPFTIING 548

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QY 249 EITFEYLKORPLAPYDSEBEWKATQYQWKNLQSPGAKYKIDVFLDAK01VPTLTWGTSP 308
Db 241 EKTIAYVKORPFPAK--GADWDAVALWRTIVSDADASPTVVEURAEPIKPOQSWGTSP 298
Db 309 EDVVPITGVYDPRDTFATRAKKAQDRRMQYMGKQAGTMDPEDIUPKVIGSCNSRIED 368
Qy 239 EMVVAIDQVQDPAAQDQDTKRSQTRQALYKMRQNPTEIHDVRVFGSCNSRIED 358
Db 429 NPDILAPQFRCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVKLADRKLTQKASPH 488
Qy 419 NPDKLGSCHCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVKLADRKLTQKASPH 488
Qy 489 IAAVQKSTTYPHYDERINQDAHEKDIADIPEDINGPHTNSAVGTA-GLPKTILK 547
Db 479 GIATSR-----HEATPSTPNRYSWMTPTQHT 507
Qy 548 GIAPPLEKANVDTAIPKQPLKTIKRTSIGNALFYEMF--NEDGTEKS----DFV 598
Db 508 GLVAPFLDRANVDTDQIIPKQFLKSKTRTGFGRPNLDEWYRVIDGSPGRNSTRPLNQEFV 567
Qy 599 LNKEPYRKASILVCTGANFGCSSREHAPWALNDFGIRSVTAPSSTADFFNNFSKNGMLP 658
Db 568 LNFPYRQGASVLLAR-ENPGCSSREHAPWALNDFGIRSVTAPSSTADFFNNFSKNGMLP 626
Qy 659 IPIKQDQAFIAAE--AAGKEIENDLPKQPLKQATGEGTCTFVEEPRKHCLNGLDD 716
Db 627 I-VLAEAENDALFQCLGIGEYQLTVDLAAQVRUPEDGVEY-AFELDAFRKHCLNGLDD 684
Qy 717 IGLTMQMEDKIAEFRAKMRRETPLDG 743
Db 685 IGLTQDADAIIGRFEGQHRAQQWPWLFG 711

RESULT 10
US 60-360-039-9413
; Sequence 9413, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
; CURRENT APPLICATION NUMBER: US/60/360,039
; FILE REFERENCE: 38-10152052/A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 9413
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(752)
; OTHER INFORMATION: unsure at all Xaa locations
; US 60-360-039-9413

RESULT 11
US 60-360-039-17883
; Sequence 17883, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10152052/A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 17883
; LENGTH: 755
; TYPE: PRT
; ORGANISM: SPHINCOMONAS
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(755)
; OTHER INFORMATION: unsure at all Xaa locations
; US 60-360-039-17883

Query Match 49.2%; Score 1995; DB 27; Length 752;
Best Local Similarity 54.8%; Pred. No. 1..e-89;
Matches 418; Conservative 96; Mismatches 207; Indels 42; Gaps 13;

Qy 9 QTLQYKVLQAHVWDEKBLGTVLILDRHLYHEVTSQAFEGCLRNACRKKVRPDCIATTD 68
Db 2 KTLQYKVLQAHVWDEKBLGTVLILDRHLYHEVTSQAFEGCLRNACRKKVRPDCIATTD 68
Qy 69 HNVPTSKRALKDIFKEDDSRQTCVUTBENKEFGVYFGLSLKRGQVHVGPEQ 128
Db 62 HNVPTSKRALKDIFKEDDSRQTCVUTBENKEFGVYFGLSLKRGQVHVGPEQ 120
Qy 129 FTLPGTTVVGDSHISTHGAFGALRGIGTSPEVETLCLITRSKNRIOQVCEELAP 188
Db 121 ATLPQMTVCGDSHISTHGAFGALANGIGTSSEVETLAVLQTLQVQKNNQVRVEGLTSLW 180
Qy 189 GVSSKQWLAHIGITGAGTGAVEFCGVIRSLMSMEARMSICMSIEGGRAGRMVAPD 248
Db 181 GVTAKD01VIALIGKIGTAGGNGYAEFGSTIRALSMEGRMTCINMAIEAGARVSKWAVD 240
Qy 249 EITFEYLKGRPLAPKDSPEWKATQYKWLQSDQGAKYDIDVFLDAK01VPTLTWGTSP 308
Db 241 EKTIQVHGRPFPAK--GSDWDAAYAFWGLVSDDAHFRVWELSAEIKPQVWGTSP 298
Qy 309 EDVVPITGVYDPRDTFATRAKKAQDRRMQYMGKQAGTMDPEDIUPKVIGSCNSRIED 368
Db 299 EMVSADVQSDQSPVDPERETDPVKKESLIRALKLTYGLONDPITSIKUDRVSCTNSRIED 358
Qy 369 IAAVQKSTTYPHYDERINQDAHEKDIADIPEDINGPHTNSAVGTA-GLPKTILK 547
Db 359 LNKEPYRKASILVCTGANFGCSSREHAPWALNDFGIRSVTAPSSTADFFNNFSKNGMLP 658
Qy 429 NPDILAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVKLADRKLTQKASPH 488
Db 419 NPDKLGSCHCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVKLADRKLTQKASPH 488
Qy 489 I-----AAYKSTTYPHYD--ERINDAHEKDIADIPEDINGPHTNSAVGTA-GLPKTILK 538
Db 477 VVFDIAWKXRANEGLYSMPPFDCFTNFTSSAXSVSKRLLFFSIP---AAXXNGSAVYRSA 532
Qy 539 G-----LPKFTILKGIAPPLEKANVDTAIPKQPLKTIKRTGLGNALFYEMF-- 587
Db 533 HRIFKWXSLSMKPFTHTGUVCPDRUVNVDQIIPKQPLKSIKRTGFGPMLPDEWRYL 592
Qy 588 ---NEDGTEK--SDPVNLKEPYRKASILVCTGANFGCSSREHAPWALNDFGIRSVIA 640
Db 593 AGQPGQDNDNSKRPINSDFVNLNPRYQGASVLLARD-NFGCSSREHAWALDYEYGRFTVIA 651
Qy 641 DSFADPFNNFSKNGMLP1PKDQOQTEAIAEARA--GKEIEVDPNQLNKNTATOTBC 698
Db 652 PSFADPFNNFSKNGMLP-VLNKVEVDALEFAQCVQTEGYFLTVLAAQVITPDGTY- 709
Qy 699 TPEVEPRKHCLNGLDDIGTQMEDKIAEFKAQMTRETLW 741
Db 710 AFQDITPRKHCLNGLDDIGTLOQEAIAFEATHRIRQWL 752

RESULT 12
 US-60-360-039-9308
 Sequence 9308, Application US/60360039
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Chen, Xianfeng
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Hinkle, Steven C.
 APPLICANT: Slater, Peter C.
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 3B-10 (52052) A
 CURRENT APPLICATION NUMBER: US/60/360,039
 CURRENT FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 9308
 LENGTH: 749
 TYPE: PRT

Matches 417; Conservative 86; Mismatches 217; Indels 48; Gaps 12; Query 9 QTYDKVLOAHVYDEKLDGTWLYIDRHLHEVTSPOAEGLENAGRAKVRPDTLATTID 68 Database 1 RTLYEKIWADHVVVERDGTCLVYIDRHLHEVTSPOAFLAGRAADRKVRPDTLAVPD 60 Query 69 HNVPTTSRKALDIASIFKEEDSRTOCUTLEENVKEFGTYFGLSDKQGQVHVIGPEGQ 128 Database 61 HNLPTTTRVDAAGNALPIADASAGOLSALRGNAEFGVPIYDALQAGQVHVVGPPQG 120 Query 129 FTLPGTIVVCGSHTSTHAGALAFGIGTSEVEHVLATOCLTRSKRMRIQVGDGELAP 188 Database 121 FTLPGTIVVCGDSHTSAHGAAGLAFGIGTSEVEHVLATOCLLQKQSTMEVRDGTGLH 180 Query 189 GYSSKDVYLHAGIIGTGTGAGVIEPGSUTRSLSMARSICNMSTEGGMAGMVPD 248 Database 181 GYSAKDVLATAGKIGAAGGTVIETFGVIRNLSEGRLTNSMSLGARSGLIAPD 240 Database 249 EITPEYLKGRLAPAKYDSPEWHAKATOWKLNQSDPGAKYDIDVFDIADIVPCLTWGTSR 308 Database 241 EKTFAYLKGRLAPLTGEA-WDRAVAYWKTLPDTDHAYTDKVTLDAADIAPISTWGTSP 298 Query 309 EDVVPITGVPDPETTATEAKKADGRMLQYQMLKAGTPMEDIPIVDKVFIGSCTNSRLED 368 Database 299 EDVVPITGVPDPQSDPSSKAAAQRSIDYQMLGTPGTAMQDIPVHEFIGSCTNSRLED 358 Query 369 LRAAAAVVKGRKCAAPNTSKAMVPGSGLVKTQAEEGLDKIFBEAGFWREAGGSMCLGM 428 Database 359 LRAAAAVQQRKVADRIEQALIIPGSLVYKROAEEGLDKIFLEAGFWREPGGSMCLAM 418 Query 429 NPDILAPQERCCASTSNINFEGRGAGGRTHLMSPVMAAAAGTVGKLAQVRLK----- 480 Database 419 NPDIKVPGERCCASTSNINFEGRGAGGRTHLMSPVMAAAAGTVGKLAQVRLK----- 478 Query 481 --TDYKASPHAAAYOKSTVTPKHDVRI-----NQDAHEKDIADIPE 521 Database 479 RGETPXRSSXHLPERXAVSPR-PMVRVTRRRSRSPRSSGSPSSRADAGGRPLPE 537 Query 522 --DNNGPHNTNTSASV-----GTSAGLPLKFTLKGIAAFLPEKANVDTAIIPQFLKTK 573 Database 538 1GDGRRPFVRAVSMYLNNTVAERRXNSRSRPARAPWGAQNIDIIIPAHWLKTT 597 Query 574 RTGLGNALFYMRFNEDGTEKSDFVNKEPKYRKAISILYCTGANFGCSSREHAPWAJNDF 633 Database 598 RIGLKGKAFFEYSR-AEPN-----LFDPPRYAGAPILY-AGENFGGSSREHAWALADM 650 Query 634 GIRSVAIAPSADIFFENNSPKNGMLPIPIKQDQIEAIAEARAKKEIIDLPHQLIKNAT 693 Database 651 GQAVLAPSDFSDIFSGNAFKNGIVTVPQEA-IDRLYQVATA-NEYITDLETMVTIDF 708 Query 694 GTTCTPFAVEFPRKHLVINGDDIGLTMQMEDKIAEFAKMTRETPWL 741 Database 709 QDRF-AFELDPFRRDCLMQLGDEIGMILAQDIAISKFESAVAHERPWI 755

Query Match 48.4%; Score 1963.5; DB 27; Length 749;
 Best Local Similarity 55.0%; Pred. No. 1.6-186;
 Matches 412; Conservative 95; Mismatches 211; Indels 31; Gaps 11;
 Query 9 QTYDKVLOAHVYDEKLDGTWLYIDRHLHEVTSPOAEGLENAGRAKVRPDTLATTID 68
 Database 4 KTLGKWLIDIEVARDDGSLLIVDRHILMEVTSPOAEGFLRGLARPLWRYNANIAITPD 63
 Query 69 HNVPTTSRKALDIASIFKEEDSRTOCUTLEENVKEFGTYFGLSDKQGQVHVIGPEGQ 128
 Database 64 HNVPTTSRKALDIASIFKEEDSRTOCUTLEENVKEFGTYFGLSDKQGQVHVIGPEGQ 122
 Query 189 GYSSKDVYLHAGIIGTGTGAGVIEPGSUTRSLSMARSICNMSTEGGMAGMVPD 248
 Database 123 ATLPGMVVCGDSHTSTHAGFLAHGIGTSEVEHVLATOCLVQVOTIDENCDDFGIFEFKMNVRQGTVHVIGPEGQ 182
 Query 189 GYSSKDVYLHAGIIGTGTGAGVIEPGSUTRSLSMEARNSICNNSIEGGARAGMVPD 248
 Database 183 GVTADIVLALIGKIGTAGGNGYAVEFSGSTIRALSEGMRNTICNNAIEGARGVNAYD 242
 Query 249 EITPEYLKGRLAPAKYDSPEWHAKATOWKLNQSDPGAKYDIDVFDIADIVPCLTWGTSR 308
 Database 243 EKTFAYLKGRLAPLTGEA-GSDMDAAVAFWGRGIVSPDPAHFDRVVLEAAEIKPQVNTGTP 300
 Query 309 EDVVPITGVPDPETTATEAKKADGRMLQYQMLKAGTPMEDIPIVDKVFIGSCTNSRLED 368
 Database 301 EMVSAVDQSPDPERETDPYKESLIRALKYMGLOQNDPPIPSKUJLRFVFIGSCTNSRLED 360
 Query 369 LRAAAAVVKGRKCAAPNTSKAMVPGSGLVKTQAEEGLDKIFBEAGFWREAGGSMCLGM 428
 Database 361 LRAAAAVVKGRKCAVSTVKQAMVPGSGLVKAQEVEGLDKIFBEAGFWREAGGSMCLAM 420
 Query 429 NPDILAPQERCCASTSNINFEGRGAGGRTHLMSPVMAAAAGTVGKLAQVRLK-----
 Database 481 SLXMIQNNVLMKVKYICCRFLVSLILAHAXSVSKRLEFFSSAAXXNGSAIYDRSVRIFK 540
 Query 540 --LPKFTLKGIAPLEKANVDTAIIPQFLKTIKRTGLGNALFYEARF-----N 588
 Database 541 HWXSLMKPFQHTGLVCPDRNVDTDQIIPQFLKSIKRTGFGPNLFDEWRYLDAGQPG 600
 Query 589 EDGTEK-----SDFVNLKEPKYRKAISILYCTGANFGCSSREHAPWAJNDF 645
 Database 601 QDNSSRKPINSDFVNLPFRYGAWSLLARD-NFGCSSREHAWALBYGFRTVIAFSFAD 659
 Query 646 IFFNNSPKNGMLPIPIKQDQIEAIAARA-GKEIEVDPNOL1KNATGETICPEVE 703
 Database 660 IFFNNSPKNGMLPIPIKQDQIEAIAARA-GKEIEVDPNOL1KNATGETICPEVE 717
 Query 704 EPRKGCLVNGDDIGLTMQMEDKIAEFA 732
 Database 718 TFRKHCLLNGDDIGLQHAEATRAFEA 746

RESULT 13
 US-60-360-039-8616
 Sequence 861, Application US/60360039
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Chen, Xianfeng
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Hinkle, Steven C.
 APPLICANT: Slater, Peter C.
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 3B-10 (52052) A
 CURRENT APPLICATION NUMBER: US/60/360,039
 CURRENT FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 9308
 LENGTH: 749
 TYPE: PRT

RESULT 14
 US-60-360-039-7437 ; Sequence 7437, Application US/60360039 ; GENERAL INFORMATION

FILE REFERENCE: 38-10 (52052)A ; CURRENT APPLICATION NUMBER: US/60/360,039 ; CURRENT FILING DATE: 2002-02-21 ; NUMBER OF SEQ ID NOS: 47374 ; SEQ ID NO 8616 ; LENGTH: 681 ; TYPE: PRT ; ORGANISM: Ralstonia metallidurans US-60-360-039-8616

Query Match 48.2%; Score 1955.5; DB 27; Length 681; Best Local Similarity 53.7%; Pred. No. 8.3e-186; Mismatches 400; Conservative 53.7%; Indels 75; Gaps 10; Matches 400; Pred. No. 8.3e-186; Mismatches 174; Indels 75; Gaps 10; Db 1 PASLDKUWASHVHIEHQSCSPLIVDRAHVNENVSPQAEGRLRJHGREWMRPAULATA 60

QY 68 DHNVPPTSRSKALKDQIASPIKEDDSRPTQCVLENTKEFGTYFGLSDKROQIVHVGPEQ 127
 QY 8 PQTQYDKVUQAHVVBKUDGTVLXIDRHJHEVTSPOATEGFLRAGRKRRPDTLATT 67
 QY 61 DHNVPTTER----AAGIDAPISRAQVDALERNCATGTVNFGMDPQGILHVGPER 114
 Db 128 GFLILPGTTWCGDSHTSTHGAGLAFAFGTSEVEHVLATOCQLIKRSKMRQVGDELA 187

QY 115 GATULPGMTIVCGDSHTSTHGAGFAFGTSEVQVLSAQCLWMKPRSLVRYVEGELA 174
 QY 188 PGVSSKDVVHAIHGTTGAGTGAIEFCCSVIRSLSMEARNSICMNSICSGARAGMV 247
 QY 175 AGUSAKDIALALIGRIGTAGATGTYIEFAGSTIRGLSMEGRMTVCNMAIEGARAGMV 234

QY 248 DEITFEYIKGRPLAPKYDSEPHWKAHQYQWVNLSQSPGAKYDIDVFDKAOIVPTLTWGT 307
 QY 235 DETTLAYLAHRPOAPOGEA--WESASAYWHTLRSIDPAVDAVVDIGVATRPHVWGT 292

Db 308 PEDVWVPTGVVDPETFAKEAKKADGRMMQYMLGKAGTPMEDIPDKVVFQGSCTNRIE 367

QY 293 PEMVVAIDERIPDRQEADEVRREMERATYMGLEPGIKVWASLADKVFQGSCTNRIE 352

QY 353 DLRRAAVVYKGKPKAVPKVSKMVVPGSLVYKTOAEEBGLKIFEEAGPENREAGSCMCLG 427

Db 368 DLRRAAVVYKGKPKAVPKVSKMVVPGSLVYKTOAEEBGLKIFEEAGPENREAGSCMCLG 412

QY 428 MNPDILAPERCSTSNSRNFGQAGGRHILMSPVMAANGIVKLADVRKLTDYKASP 487

Db 413 MNDDRLAPERCSTSNSRNFGQAGGRHILMSPVMAANGIVKLADVRKLTDYKASP 462

QY 488 HIAVYQKSTVTKPHYDERINQDAHEKDIADIPEDNINGPHTNTSASVGTSAGLPKTILK 547

QY 463 -----STVQ-----EK-----SAVAKTVL 479

Db 548 GIAAPLEKANVDTAIIPKPLKTKRTGIGNAYFEMRENEDG-----TEKSDFV 598

QY 480 GLVAPIDRANVDTAIIPKPLKTSQRSRGPYLPFEEWRVYDPPGERGQDCSQRPNPDFV 539

QY 599 LNKPYRKASSILVCTGANCFCGSSREHAPMALDFGTRSVTAPSADIFNNFSKQMLP 658

Db 540 LNQPRYQGASVLL-VRENFGCSREHAPMLEDGFLRALLAPSADIFCNMKGQLLP 598

QY 659 IPIKQQAQIRAAE--ARAGKEIEVDPNQLNLIKATGETCTFEEVEEFKHCVLNGLD 716

QY 717 IGLTMQMEDKIAEFAKMTBTTPWL 741

Db 657 IGLALQHEREEIRRVEALRNPWEL 681

QY 649 NNSFKNGMPLPIKQQAQTEAIAARA--GKEIEVDPNQLNLIKATGETCTFEEEF 706

Db 647 NNCFKNGVLPVILVTEQ-QVDHLENEYTAENGKFLTVLDAQVVRADGGTEYFPEVAER 705

Query Match 46.6%; Score 1891; DB 27; Length 740; Best Local Similarity 52.5%; Pred. No. 2.9e-179; Mismatches 396; Conservative 52.5%; Indels 62; Gaps 13; Matches 396; Pred. No. 2.9e-179; Mismatches 195; Indels 62; Gaps 13; Db 34 DRULVHEVTSPOATEGFLRAGRKUR---RPDTIATDHNVPPTSRSKALKDIAFIKED 89

QY 150 GALAFGIGTSEVEHVLATOCQLIKRSKMRQVGDELAHPGVSSKDVVHAIHGTTGAGT 209
 Db 113 GALAHGIGTSEVEHVLATOCQLIKRSKMRQVGDELAHPGVSSKDVVHAIHGTTGAGT 172

QY 90 DSRTQCVLENTKEFGTYFGLSDKROQIVHVGPEOFTLPGTWTWCGDSHTSTHGAF 149

Db 53 ISRLQVDTLSDNCDAYGTFQKMDRQGIVHIGPEQATLPMNTIVGDSHTSTHGAF 112

QY 210 GAVIFCSCVIRSLMEARNNSICMSIEGARAGMVAPELTFKLGSLPLAPKDXPEN 269

Db 173 GYALFGGSTIRALSMEGRMVTVCNMAIEGARAGMV 230

QY 270 HKATOQYWNLSQSPGAKYDIDVFDKAOIVPTLTWGTSPEDWVITGTVVDPETATEAK 329

Db 231 NHAVYKQPKSDDDGAOFDRVVELNRAEIVPOQVITGWTSPENMVTDGVPDPDKPVK 290

QY 330 KADGRMLOYMLGKAGTPMEDIPDKVVFQGSCTNRIEULRAAAVVK--GRKPKAVPK 387

Db 291 RDALERAKYMAEPNAPIESKPKDIFIFIGSCTNRIEIDIRAAVVKLGRVAPNIRL 350

QY 388 AMVUPGSGLVIKTOBEEGDKTIEBEGFMRREAGSCMCGMNPDLAPERCSTSNSRN 447

Db 351 AMVUPGSGLVIKTOBEEGDKTIEBEGFMRREAGSCMCGMNPDLAPERCSTSNSRN 410

QY 448 EGROGAGRTHLMSPVMAAAGIVKLADVRKLTDYKASPHTAAVYOKSTVTK----- 499

Db 411 EGROGAGRTHLMSPVMAAAGIVKLADVRKLTDYKASPHTAAVYOKSTVTK-----NRTLLRRAFGSLA 467

QY 500 -----PHVDERINQDAHEKDIADIPEDNINGPHTNTSASVGT 539

Db 468 GLLIGLAGNTVHGGEDMSHGNISINHADKXAVDFGRPAQGGFXSLRASCGLETG 527

QY 540 --LPKFTLKGIAAFLPEKANVDTAIIPKPLKTKRTGIGNAYFEMRENEDGTEK 594

Db 528 SVMEKFIVTGVVAPLDRENVDIDAIIPKPLKTSKRTGFGPNAFDEWRVLDHGPQDN 587

QY 595 S-----DVLNKPYRKASSILVCTGANCFCGSSREHAPMALDFGTRSVTAPSADIF 648

Db 588 SORPLNPDFVLNQPRYQGASVLL-KNFGCGSSREHAPMALDFGTRSVTAPSADIF 646

QY 649 NNSFKNGMPLPIKQQAQTEAIAARA--GKEIEVDPNQLNLIKATGETCTFEEEF 706

Db 647 NNCFKNGVLPVILVTEQ-QVDHLENEYTAENGKFLTVLDAQVVRADGGTEYFPEVAER 705

Query Match 46.6%; Score 1891; DB 27; Length 740; Best Local Similarity 52.5%; Pred. No. 2.9e-179; Mismatches 396; Conservative 52.5%; Indels 62; Gaps 13; Matches 396; Pred. No. 2.9e-179; Mismatches 195; Indels 62; Gaps 13; Db 53 ISRLQVDTLSDNCDAYGTFQKMDRQGIVHIGPEQATLPMNTIVGDSHTSTHGAF 112

QY 150 GALAFGIGTSEVEHVLATOCQLIKRSKMRQVGDELAHPGVSSKDVVHAIHGTTGAGT 209
 Db 113 GALAHGIGTSEVEHVLATOCQLIKRSKMRQVGDELAHPGVSSKDVVHAIHGTTGAGT 172

QY 90 DSRTQCVLENTKEFGTYFGLSDKROQIVHVGPEOFTLPGTWTWCGDSHTSTHGAF 149

Db 53 ISRLQVDTLSDNCDAYGTFQKMDRQGIVHIGPEQATLPMNTIVGDSHTSTHGAF 112

QY 210 GAVIFCSCVIRSLMEARNNSICMSIEGARAGMVAPELTFKLGSLPLAPKDXPEN 269

Db 173 GYALFGGSTIRALSMEGRMVTVCNMAIEGARAGMV 230

QY 270 HKATOQYWNLSQSPGAKYDIDVFDKAOIVPTLTWGTSPEDWVITGTVVDPETATEAK 329

Db 231 NHAVYKQPKSDDDGAOFDRVVELNRAEIVPOQVITGWTSPENMVTDGVPDPDKPVK 290

QY 330 KADGRMLOYMLGKAGTPMEDIPDKVVFQGSCTNRIEULRAAAVVK--GRKPKAVPK 387

Db 291 RDALERAKYMAEPNAPIESKPKDIFIFIGSCTNRIEIDIRAAVVKLGRVAPNIRL 350

QY 388 AMVUPGSGLVIKTOBEEGDKTIEBEGFMRREAGSCMCGMNPDLAPERCSTSNSRN 447

Db 351 AMVUPGSGLVIKTOBEEGDKTIEBEGFMRREAGSCMCGMNPDLAPERCSTSNSRN 410

QY 448 EGROGAGRTHLMSPVMAAAGIVKLADVRKLTDYKASPHTAAVYOKSTVTK----- 499

Db 411 EGROGAGRTHLMSPVMAAAGIVKLADVRKLTDYKASPHTAAVYOKSTVTK-----NRTLLRRAFGSLA 467

QY 500 -----PHVDERINQDAHEKDIADIPEDNINGPHTNTSASVGT 539

Db 468 GLLIGLAGNTVHGGEDMSHGNISINHADKXAVDFGRPAQGGFXSLRASCGLETG 527

QY 540 --LPKFTLKGIAAFLPEKANVDTAIIPKPLKTKRTGIGNAYFEMRENEDGTEK 594

Db 528 SVMEKFIVTGVVAPLDRENVDIDAIIPKPLKTSKRTGFGPNAFDEWRVLDHGPQDN 587

QY 595 S-----DVLNKPYRKASSILVCTGANCFCGSSREHAPMALDFGTRSVTAPSADIF 648

Db 588 SORPLNPDFVLNQPRYQGASVLL-KNFGCGSSREHAPMALDFGTRSVTAPSADIF 646

QY 649 NNSFKNGMPLPIKQQAQTEAIAARA--GKEIEVDPNQLNLIKATGETCTFEEEF 706

Db 647 NNCFKNGVLPVILVTEQ-QVDHLENEYTAENGKFLTVLDAQVVRADGGTEYFPEVAER 705

Qy 707 KHCLVNLDDIGITMQMEDKIAAPEAKMTRTETPWL 741
 Db 706 KYCLLNGFDDIGLTLRHDKIRQFEAERTAKQPNL 740

RESULT 15
 US-60-360-039-4678 ; Sequence 4678, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; NUMBER OF SEQ ID NOS: 47374
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10-(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; PRT: PRT
 ; ORGANISM: Burkholderia fungorum
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1). (729)
 ; OTHER INFORMATION: unsure at all Xaa locations
 US-60-360-039-4678

Query Match 46.4%; Score 1881; DB 27; Length 729;
 Best Local Similarity 52.5%; Pred. NO. 2.8e-178; Indels 88; Gaps 13;
 Matches 396; Conservative

Qy 46 AFGGLRNAGRKVYRPRDCTLATTDHNVPTTSRALKDIASFIKEEDSRTOCVTLEENVKEF 105
 Db 4 AFFA-EAAERPWIRISANLSDHNVPTDR----SHGIAADPISRLQVDTLDSNCNDAY 56

Qy 106 GVFYFLGSDKRCGIVHVTGPEQGFTLPGTNTVCDSHPTSTHGAGLAFGIGTSEVEAVL 165
 Db 57 GITQFKNDLRLRQGIVHVTGPEQATLPGMTIVCDSHSTSTHGAGLALHGIGTSEVEHVL 116

Qy 166 ATOCLTTRKSNNMRIOVGDGEALPGVSSKDKDVHLHAIGITGAGTGTGAVTEFGSIVTRSLM 225
 Db 117 ATQTLRQSKNMLVKVAGALPQGCTARDIVLTTIGKIGTAGGIGYATBFGGSTIRALM 176

Qy 226 EARMSTCNMSIEGARAGMVAPEBITEFYKLGRPLAKYDSSPEMKATQYWKLNQSDPQA 285
 Db 177 EGRMTVCNMAIEGARAGMVAQDFTTILYKLGRPFSP--EGVWVNHAVEYWKQFKSDDCA 234

Qy 286 KVIDVFDIADKVPLTWTGSPDIDVLTGVDPETPATEAKDRGRMLQMGKXAG 345
 Db 235 QPDRVVELNAAEVQPOVWTGSEMMVTAVGTVYDGRVDPDREKPKYKRDALERALKYMALEPN 294

Qy 346 TMDPIDIYDVKFVGSCTNRIEDIRAAAVK--GRKEKAPVNSAMVYFGSLVKTQAE 403
 Db 295 APEISIPDKIFGSCTNRIEDIRAAAVK--GRKEKAPVNSAMVYFGSLVKTQAE 354

Qy 404 EGSLDKIFEEAGFWRAGCSMCLGMNPDLAQERCASTSNRNFEGRQAGGRTHLMSPV 463
 Db 355 EGSLDKVETDAGFWRAGCSMCLAMNDRLEPGERCASTSNRNFEGRQAGGRTHLVEPA 414

Qy 464 MAAGIYGKADVRKLTDYKASHP-----IANYQST 476
 Db 415 MAAAAGAIAEGHFDIRKLGXTRMMKNNMRTTLLRRFALGSLAGLILGLAGCTVARIIGH 474

Qy 497 VTKPHYDER-----INDQDAHEKDITIADIPEDNNNGPHNTSASVTS 537
 Db 475 VARPROFQDQSRRXISGXFPLAMPKKAFAFSRCARH-----PGLFGASV-- 518

Qy 538 AGLPKFTILKGIAAPEKANVDTDAIIPKQFLKTIKRTGLGNALFYENRF--NEDGTEK 594
 Db 519 -MEKFIVHTGVVAPLDRENVDTDAIIPKQFLKSIRTGFPNAFDEWRYLHGEPOQN 576

Qy 595 S-----DFVLNKEPYRKASILVCTGANTFGCSSLRSHAPWALNDFFGIRSVIAPSFAIDIFF 648
 Db 577 SQRPLPDFVLNQPRVGASVLLAR KNFGCSSLRSHAPWALEQYGRALLAPSEADFY 635

Qy 649 NNSFKGMLPLPIKODAQATEAAERA--GKEIEVDLPNOLKNTGETCTFEYBEFR 706
 Db 636 NNCFCRNGVLPVLTED-QVDILFNEYAFNFGFLKTVLTDQAVTRDGTEYTFEVAFR 694

Qy 707 KHCLVNLDDIGITMQMEDKIAFEFKMTRTPWL 741
 Db 695 KYCLLNGFDDIGLTLRHDKIRQFEELERIAKQWL 729

RESULT 16
 US-60-360-039-7055 ; Sequence 7055, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10-(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 7055
 ; LENGTH: 686
 ; TYPE: PRT
 ; ORGANISM: Burkholderia cepacia
 US-60-360-039-7055

Query Match 45.9%; Score 1861; DB 27; Length 686;
 Best Local Similarity 51.5%; Pred. NO. 2.6e-176; Indels 188; Gaps 11;
 Matches 387; Conservative 94; Mismatches 188; Indels 82; Gaps 11;

Qy 6 STPQTLYDKVILQAHVYDEKLQDGTWLLYIDRHLVHEVTSPOAEGFLNAGRKVYRPRDCTLA 65
 Db 3 TSPTRLQDQLWQSHVVAETPRGPFLYDVRHLVHEVTSPOAFAEALRSGRKPRPETYVLA 62

Qy 66 TTDHNVPPT----TSRKALDIASFIKEEDSRTOCVTLEENVKEPYTYFGSLDKRQGIV 120
 Db 63 VADHNVPPTAAERTSDMADPL----SRIQVBLQDKNCKEPLGKSYGIRNPQGII 115

Qy 121 HVIGPQGFTLPGTIVVCGDSHTSTGAGFALAFGIGTSEVEHVLATQCLTTRKSNNMR 180
 Db 116 HVVGPFLGATLPGMVTVAGDSHTSTGAGFALAFGIGTSEVEHVLATQCLSVGKMSMLV 175

Qy 181 QVDEGELAPGVSSKDKDVLHATGIGTAGGTGAVIEPGSIVRSLSMARMMSICNMSLEGGA 240
 Db 176 NVEGVLPVGVTAQDVLATIIRRGTGAGTGYAMEFFGSTRTLSMGRMTLCNMAEAGA 235

Qy 241 RAGMVPADETFEYKLGRPLAKYDSDPEWIKATQWKNLQSDPQAKYDIDVPAIDIVP 300
 Db 236 RVGLIGCDDVTTIDYVYGRPFAPA--EAHWDAAVYRTLVEDDAADFQKVNIDATOLRP 293

Qy 301 TLTWGTSPEDVVPITCVPDPETFATEAKKADGRMLQYNGSLKAGPMPEDIVPDVKPFTGS 360
 Db 294 MVTWGSTSPMVTVDDAVPNPLDDPPPVYRATMAGLTYMGLEPGTSLSKISLSDKFTGS 353

Qy 361 CTNSR1EDIRAAAVTVKGRKAPNVTAMVPGSIVKVKQAEEGIDK1FEEAGFVRE4A 420
 Db 354 CTNAR1EDIRRAAAATVKGHRVAPYVQLAVPGSGLIVKAQREAGELDAIFKEAGFVREP 413

Qy 421 GCSMCIGMNPDLAQERCASTSNRNFEGRQAGGRTHLMSPVMAAAGTGVKLADYRKL 480
 Db 414 GCSMCIGMNDRLPERCASTSNRNFEGRQGGSHLVSPPAAAATAGHFVIVD-- 470

Qy 481 TDYKASHPIAAVQKSTVTKPHVDERINQDAHEKDITIADIPEDNNNGPHNTSASVGSAGL 540

RESULT 17
 US-60-360-039-4299
 ; Sequence 4299, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-101520521A
 ; CURRENT APPLICATION NUMBER: US/60/360, 039
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 4299
 ; LENGTH: 688
 ; TYPE: PRT
 ; ORGANISM: Burkholderia fungorum
 ; US-60-360-039-4299

Query Match 45.8%; Score 1857; DB 27; Length 688;
 Best Local Similarity 51.3%; Pred. No. 6.6e-176;
 Matches 386; Conservative 92; Mismatches 189; Indels 86; Gaps 10;

QY 6 STPQTYDVKVQAHVDEKLDGTWVLYTDRHIVHEVTSQATEGLRNAGRKVRRPDCTLA 65
 Db 5 TSPRTLILDKLWOSHVVAEATPNTGPTLIVDRHIVYEVTSQATEGLRNAGRKVRRPDCTLA 64

QY 66 TTDHNHPT----TSLKALKDASFIKEDDSRTOCVTILEENKEFGTYFGSLSKQGIV 120
 Db 65 VADHNVPTTAERTSMDAIDPL----SRIQAOGLDKNCKFGIKSYGRNPNQOGII 117

QY 121 HVIGPEOCCFTLPGTVCGDSHTSTHGARGALAFGIGTSEVERVLAQTOCLITKRSKOMRI 180
 Db 118 HVVGPGLGATLPGMTWVAGDSHTSTHAGAALAFGVGTSEVERVLAQTOCLSTVGMKMLV 177

QY 181 QVGDGEALPGVSSKDVIRAIAGITGAGTGTGAVIEFCSSVIRSLSMEARMSICNMSLGGGA 240
 Db 178 NVEGLVLPVGVTAKDVLIAIRRGTAGGTGYAMEFAGSSTIRLSEMEGMLTICMNAIEAGA 237

QY 241 RAGMVADEDEITBEYLKRPPLAKYDSEPHWKATOQWKLQLOSPGAKYDIDVFDADKOVIP 300
 Db 238 RVGLIGVVDVDTIDYVKGPFPAPA-EAHWDAAVAYWRITLVSDARFDKIVNIDATORLP 295

QY 301 TLTWGSPPEDVPUITGVVDPDPETFATEAKKADGRMRMQLQYMGKLAGTPEMDIVDKVIGS 360
 Db 296 MYTWGTSPEMUVVTFDADVPNPLDPPVRATMAGALTYMGLPPTSLKSISLDKLFIGS 355

QY 361 CTNSRFLDRLAAMAVVKGKKAAPNPKSAANVPGSGLYKIQABEGGLDKLIFEGAFENREA 420
 Db 356 CTNARIELRLAAMAVVKGKKAAPNPKSAANVPGSGLYKIQABEGGLDKLIFEGAFENREA 415

QY 421 GCSMCLGNPNDLAPQERCASTSNRNFGRGQAGGRTHLMPVMAAAGIVGKLADVRKL 480

RESULT 18
 US-60-360-039-9059
 ; Sequence 9059, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-101520521A
 ; CURRENT APPLICATION NUMBER: US/60/360, 039
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 9059
 ; LENGTH: 672
 ; TYPE: PRT
 ; ORGANISM: Chloroflexus aurantiacus
 ; US-60-360-039-9059

Query Match 42.2%; Score 1711.5; DB 27; Length 672;
 Best Local Similarity 49.2%; Pred. No. 2.6e-161;
 Matches 358; Conservative 97; Mismatches 210; Indels 63; Gaps 12;

QY 8 PQTLYDKULQAHVW-DEKLDGTWVLYTDRHIVHEVTSQATEGLRNAGRKVRRPDCTLAT 66
 Db 1 PRTLFKEWHAHLVRPETAETPAVLYIDLHLTHEVTSQATEGLRNAGRKVRRPDCTLAT 60

QY 67 TDHNVPTTSRALKDASFIKEDDSRTOCVTILEENKEFGTYFGSLSKQGIVHWIGP 126
 Db 61 MDHSTPTPRNHGIP-VVDPMAISQLEQLRKNCAEFGIPLFELGDENGQIVHWIGP 118

QY 127 QSTTLPGTIVWGGDSHTSTHGARGALAFGIGTSEVERVLAQTOCLITKRSKOMRI 186
 Db 119 QGJITQGPMTIVEGDSHTSTHGARGALAFGIGTSEVERVLAQTOCLQRPKTCAVRIGRL 178

QY 187 ACVSSKDVULHAIGIIGTAGCTGAVIEFCSSVIRSLSMEARMSICNMSLGGGA 246
 Db 179 GRTVTAODITLALIAKYGVGGGTYVFEYMGBAIRALSMEERMTCNSMIEGGRAGMVA 238

QY 247 PDETFEYLKGPLAKYDSEPHWKATOQWKLQLOSPGAKYDIDVFDADKOVIPWGT 306
 Db 239 PDDTFEYLKGPLAKYDSEPHWKATOQWKLQLOSPGAKYDIDVFDADKOVIPWGT 296

QY 307 SPEDVPUITGVVDPDPETFATEAKKADGRMRMQLQYMGKLAGTPEMDIVDKVIGS 366
 Db 297 NPGMGIPIADPPVRPDPMDPDRSRAALDKALYMLQYMGKLAGTPEMDIVDKVIGS 356

Qy	367	EDLRAAAVVKGRKIKAPNVKAMMVPGSGLYVTKQAEGLDKEEAGFEEAGFEEAGCNSMCL 426	Qy	249	BITFEYLGGRPLAPKVDSPWHEKATQWKNLQDGPQAKYDIDVFDKADIVPLTWGTPSP 308
Db	357	SDLRQAAFFGRKVYAPGVR -VMVVPSSQVRAAEAEGLDR FKEAGAEWRAAGCSACL 415	Db	235	ETTFENYIKGRREFAPK --GAKNDEAVAWKWTLYSDSDAVFDKLYDAADIGPMITYGTNP 292
Qy	427	GMPNDLILAPQERCASTSNRNFGRQAGGRTHLMSPWNAAAGIVGKLADEVRLKTDYKAS 486	Qy	309	EDVVPITGVVDPETPATEAKKADGRMLQINGLKGATGTPMEDIIPDVKVFIGSCTNSRIED 368
Db	416	GMDDKVKPPGKYYAVSTSNRNFGRQAGGRTHLMSPWNAAAGIVGKLADEVRLKTDYKAS 486	Db	293	GMGIVSNKRNISPLDSI EESNKVTFNKAALDINGFHAGDSLIGKVNWVFLGSCTNRIED 351
Qy	487	PHIAAYQKSTVTKPHYDERTINDAHEKDIADIPDENGPHNTNTSASVGTAGLKPFTIL 546	Qy	369	LRAAAVVKGRKIKAPNVKSAVMYPGSSCLVKTQAEEGLDKIFEEAGFEEWREAGGSMCLGM 428
Db	467	AHVVLEEAHV -	Db	352	LROFAFFVKGRGOKAANT -NALIVPGSKCOVEKQIAEGIDKVLAEEAGFELREPAGSCLAM 410
Qy	547	KGIAAPLEKANVDTDAIIPKQFLKTKTGTGLNQALFYEMRFNEDGTEKSDFVLINEKEPRK 606	Qy	429	NPDLAPQERCASTSNRNFGRQAGGRTHLMSPVMAMAGIVGKLADEVRLKTDYKASPH 488
Db	486	KAVVLVPE -NIDTDQIIPARLKVTDGRSGIAAGLFEFAWRYQADGTPNIPDFPLNRPEAG 543	Db	411	NEDKVPKGECYVSTSNSNRFGRQGPGRLLVSPLTAAIAVSGKIVDREMNXNSNIQ 470
Qy	607	ASILVCTGANFGCGSREHAPWALNDGIRSVTAPSADIFFNNSFKNGMLPPIKDOAQ 666	Qy	489	IAAYOKSTVTKPHVDRBLINODAHEKDIADIPDENGPHNTNTSASVGTASAGLKPFTILKG 548
Db	544	ATILLI-SGRNFQCGSSREHAPWALQDGFKAVALSPADIFNSNSLKGILPPTI-DOAV 601	Db	471	ISFIKR -
Qy	667	IEIAAAEARAGKE -IEVDLPNQLNKINATGETCTFEEPFKHLVYNGLDIGLTMOME 724	Db	474	-IPRTMEEKFITIKS 494
Db	602	YDELVARYAAADPMQMLTIDLATQTVTLPLDGRAY-HFPIDAFSKYCLLHGVDQFLLQCE 660	Qy	549	IAAPLEKANVDTDAIIPKQFLKTKTGTGLNQALFYEMRFNEDGTEKSDFVLINEKEPRKAS 608
Qy	725	DKIAEEA 732	Db	495	TVVPLPIEDVDTQIIPARLKATTKGKFGKSLFCDMRYNODGTPKADVMN NPLYSGQ 553
Db	661	EAIIAYEA 668	Qy	609	ILVCTGANFGCGSSREHAPWALNDGIRSVTAPSADIFFNNSFKNGMLPPIKDOAQ -QA 665
Qy	RESULT 19	US-60-360-03-9-10463	Db	554	ILV-AGKNGCGSSREHAAWAGDAGRRVVVSSFFAD FRGNALNNGLPVQVSDAFLKS 612
Qy	SEQUENCE 1 0463, Application US/60360039	Qy	666	QIEATAEARAGKEIIVDLPNQLNKINATGETCTFEEPFKHLVYNGLDIGLTMQMD 725	
Qy	GENERAL INFORMATION:	Db	613	IFDAVANAK -QELVYDLANQVISIAGTDLKRESFVINEYKCTCLINGYDDIVLVIKSIKD 670	
Qy	APPLICANT: Cao, Yongwei	Qy	726	KIAEFE 731	
Qy	APPLICANT: Chen, Xianteng	Db	671	KIEAYE 676	
Qy	APPLICANT: Goldman, Barry S.	RESULT 20	US-60-360-039-16643		
Qy	APPLICANT: Hinkle, Gregory J.	GENERAL INFORMATION:	US-60-360-039-16643		
Qy	APPLICANT: Slater, Steven C.	APPLICANT: Cao, Yongwei	Sequence 16643, Application US/60360039		
Qy	TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES	APPLICANT: Chen, Xianteng	APPLICANT: Goldman, Barry S.		
Qy	FILE REFERENCE: 38-10(52052)A	APPLICANT: Hinkle, Gregory J.	APPLICANT: Hinkle, Gregory J.		
Qy	CURRENT APPLICATION NUMBER: US/60360039	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	CURRENT FILING DATE: 2002-02-21	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	NUMBER OF SEQ ID NOS: 47374	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	LENGTH: 676	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	TYPE: PRT	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	ORGANISM: Cytophaga hutchinsonii	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	FEATURE: NAME/KEY: unsure	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	LOCATION: (1) ..(676)	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	OTHER INFORMATION: unsure at all Xaa locations	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	US-60-360-039-10463	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	Query Match 9	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	Best Local Similarity 41.9%; Score 1697.5; DB 27; Length 676;	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	Best Local Similarity 48.5%; Pred. No. 6 6e-160; Mismatches 352; Conservation 109; Gaps 10;	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	Matches 352; Conservation 109; Mismatches 212; Indels 53; Gaps 10;	APPLICANT: Slater, Steven C.	APPLICANT: Slater, Steven C.		
Qy	9 QTLYDKVLOHVYDBKLDTGTVLILYDRLHLYHTSPOQAEGIIRNAGRKVRPDCLTATTD 68	Query Match 9	41.5%; Score 1692.5; DB 27; Length 646;		
Db	1 KTLFIERKWNAAHVVTYKDGPSLILYDRLQHHTVTSPOQAEGIIRKRGCVFRPRTLATTD 60	Best Local Similarity 49.7%; Pred. No. 1.9e-158; Mismatches 359; Conservative 87; Gaps 81;	Best Local Similarity 49.7%; Pred. No. 1.9e-158; Mismatches 359; Conservative 87; Gaps 81;		
Qy	69 HNVPTTSRKALKDIAFIKEEDDSRITQCVTLEBNVKEFVGTYGLSDKRGQIYHVGPGQ 128	Qy	11 LYDKVLOHVYDBKLDTGTVLILYDRLHLYHTSPOQAEGIIRNAGRKVRPDCLTATTDH 70		
Db	61 HNVPTKGONLP----IVEDLSRQFVDKLTENCNKEFVGTVLGLHAGSQVHVVGPGT 114	Db	5 LLDKWUERHVVATNENGLDLYDILHLYHTSPOQAEGIIRNAGRKVRPDCLTATTDH 64		
Qy	129 FTLPGTTVCCGDSHTSTHGAFALARGITSEVEHVLATOCILITKRSKRNMRQYDGELAP 188	Qy	71 VPTTSRKALKDIAFIKEEDDSRITQCVTLEENYKEFGTYFGLSDKRGQIYHVGPGQFT 130		
Db	115 TLPGNTIVCCGDSHTSTHGATGSIAGTSEVEQVLAQCMOTKATLKBEINGKAK 174	Db	65 IPT----IDTRIAKQQLDTPRENCKQFQPLADIGDEEQVHVVGPGELGLT 117		
Qy	189 GVSSKDQVVLHAIGIGTAGGCGAVIFCGSVTRSLMSBMAEWSNCMSIEGGRAGMYAPD 248	Qy	131 LGTTIVWCGDHSITSTHAFGALAFGTCSEVHLATQCLITRSKRNMRQYDGELAPV 190		
Qy	175 GVTAKDVLVIAQI SAAGGTGCFYVYCGSAATLSNEARMTICNMSIEMGRGGMIAFD 234	Db	;		

118 OPGKTIIVGGDSHTATHGAGFALAFGTSSEVERVLTATWORKPKAAGIELKGLKLUPOGV 177

QY 191 SSKDVLVHLAIGIIGTAGGTGAVIEPCGSVIRSLSMARMSICNNSIEGGARAGWAPDEI 250

Db 178 YAKDILHLSSKYGVAVGTTGVMFYGCAEHAMDEEMTLCNWAIBSGAKAGITAPDEK 237

QY 251 TFEYIKGRPLAKYDSEPEWHRKATQYWNKLQSPGAKYIDVFDIADKVLTPTGTSPE 310

Db 238 TVAYVKGRKYAPK---DYESTKKKWSSELYTDADYVHILVUTDAPYVGTNPMS 293

QY 311 WPTITGWPDPETFATRAKKADGRMRQYQMGKAGTPEDIPIPKUF GSCNTNSRIEDR 370

Db 294 GVRIDBKLP-----EKHDANDERAFSYMSYGMSPGQSTYDIPVQHVFQGSCNTNRLSD 346

QY 371 AAAAVVKGRKKGAPVNSAMVPGSGLYVKTQAEERGLDKEFPEAGFWRAGCSMQLGMNP 430

Db 347 IAASTVKGKVKOEGVR-AVUVGSQRTREAMHKGHLIFEEAGFWRERPGCSMQLGMNP 405

QY 4331 DILAPOERCASTSNRNFEGROGAGGRTHLMSPVMAAGIVGKLAADVRLTDYKASPHIA 490

Db 406 DQVPGEGHCASTSNRNFEGROGKARTHLVSPAMAAALYGHFUDRK----- 454

QY 4931 AYQKSTVTKPHUDERINQDAHEKDIAIDIPEDNNGPHNTSASVGTASAGLPLKFTLKGIA 550

Db 455 -----ESTHDG-----AFRIHKGT 468

QY 551 APLEKANDTDIAIPKOFFLTIKRTGLGNALFYEMRFPEDGTEKSDPVLNKEPYKASIL 610

Db 469 AVLMDUNIDTPQIIPKQYKLRERTGGKFLEDEWRYNNRQENPNPFLNAQERKGASIL 528

QY 611 VCTGANFGCCSSREHAPWALNDFGIRSVIAPSADIFFNSFKNGMLPIKDKQQIEAI 670

Db 529 i-TGDNFGCGSSREHAPWALADYGFYVIIAGGFADIFVNCMKGMLPI-VMDKDMRQL 586

QY 671 AAEAAEAGKEIENDPLNOLIKATGETCTTFFEVFPRKICLVNGLDIGITQMDKIAEF 730

Db 587 -AKTDAREQITDLEMIBMTNTHR - FHPFTERKWKSEKLUINGLDIBISTMVOQIEKEY 643

QY 731 EAK 733

Db 644 ERK 646

RESULT 21

US-60-360-039-14041 Application US/60360039

; Sequence 14041, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SBO ID NO: 1441

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Pseudomonas fluorescens

; FEATURE: NAME/KEY: unsure

; LOCATION: (1)..(679)

; OTHER INFORMATION: unsure at all Xaa locations

US-60-360-039-14041

RESULT 22

PCT-US02-03987-5730

; Sequence 5730, Application PCT-US0203987

; GENERAL INFORMATION:

; APPLICANT: Elitra Pharmaceuticals, Inc.

; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C

; TITLE OF INVENTION: Proliferation

; FILE REFERENCE: ELITRA-08VPC

; CURRENT APPLICATION NUMBER: PCTVUS02/03987

; CURRENT FILING DATE: 2002-02-02

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 1581

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 5730

LENGTH: 644

TYPE: PRT

ORGANISM: Staphylococcus aureus

FEATURE: NAME/KEY: VARIANT

LOCATION: (1)..(644)

Query Match 41.2%; Score 1670.5; DB 27; Length 679;

Best Local Similarity 47.3%; Preid. No. 3.4e-157;

Matches 355; Conservative 108; Mismatches 209; Idents 79; Gaps 15;

QY 9 OTLYDKULLQAHV--DEKLGDGVLLYKDRHLVHEVTSPQAPEGIRNAGRVRDRDCTLA 65

Db 1 RTLYKHDTSHTVCTLDDQ--GHVILYDQVANEITSQARESGUREAGRTWPRPAATLA 58

QY 66 TTHNRPVTPSRKALDIASFIKEDSRSTQCTVTEENKEFVFTYFGSLDKROGVHVTG 125

Db 59 VVDRVNPT---APKRIATWPDAGGAR-QVSYFEENCRDFGFLBLFDVLDRQGIEHVWAP 113

QY 126 EQTITLGPGTIVVCCDSHTSHGACGALAFCTGTSVHEVHLATQCLITKRSKNNRQDGE 185

Db 114 EQGFLPGMVNAQDSHTT'YGAJGAFGEGTGTSEEHLLATOTLVYKRLKLTUVTNGE 173

QY 186 LAEGVSKVVLHAIGIIGTAGGICAVIEPCGSVIRSLSMARMSICNNSIEGGARAGV 245

Db 174 LGAGVTSKQIMAJEKIGASGATGIAEFTGPAISALSVARMTNMAVAGARAFM 233

QY 246 APPBITEYIKGRPLAKYDSDPEWHRKATQYWNKLQSDPGAKXKIDVFDIADKOUVPTLJW 305

Db 234 APPDKVFAVILQHKPRAPK--GKLMEOQADHWTKLHSDEAVFREVILDVALELPMVW 291

QY 306 TSPEDWVPTGVPDPETATEAKKADGEMLYQWYMLKAGTPMEDIPIVDKVUTGCSNR 365

Db 292 TSPDQAAPIKAHVDPDAOPDPTIROLGLRQLADYMLITPGMLPNLVNTISHAFGSCNAR 351

QY 366 IEDIRAAAVVKGRKKGAPVNSAMVPGSGLYVKTQABEGLDFKIFEEAGFWRAGCSMC 425

Db 352 IEDIRDVARVGRGKVAATR - AMI VPGSTI VTRNQADEGIAQIFLDAGFENRQSGCSMC 410

Db 455 -----ALEAXT-----MQPDT 476

QY 546 LKGNTAAPPLEKANTDIAIPKOFFLTIKRTGLGNALFYEMRFPEDGTEKSDPVLNKPYR 605

Db 477 VSSAAPEFLASNIDTDVIMKOFKLGIDRQGLDFDLRFLASGEBNPEVLNQPAWO 536

QY 606 KASLIVCTGANFGCCSSREHAPWALNDFGIRSVIAPSADIFFNSFKNGMLPIKQDQ 665

Db 537 DAATLV-TGPNFGCGSSREHAPWGLKQVGLAIGITFAGFYYDNCRNGVIAIQL-DDA 594

QY 666 QI---EAEEAAEAGKEIENDPLNOLIKATGETCTTFFEVFPRKICLVNGLDIGITM 721

Db 595 QFRKVAEATSVPATA - RISVNLQATLELADG-TLIEFEDQLRKQSLILGDAITL 651

QY 722 QMEDKIAEBAKMTRETPWLDGTVLKRKGQ 752

Db 652 QRTBQIRAFEARHLADNPML--GZQWQNGR 679

OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-01987-5730

Query Match 41.1%; Score 1666.5; DB 1; Length 644;
Best Local Similarity 48.7%; Prd. No. 7.0e-157; Gaps 10;
Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10;

Oy 9 QTLYDKVLAHQHVVDEKLDGTVALYIDBHLVHEVTSQAPEGLENAGRKVRPDCTLATTID 68
Db 3 QTLFDKVWNRHVLYKGIGEPLQLYIDHLHLEVTSQAPEGLRLQNLKLRPLTFTALD 62

Oy 69 HNPVPTSRKALKDIASTPIKEDDSRTOCVTLEENVKERGTVYFGLSDKROQGIYHVGPEQ 128
Db 63 HNPVPTI----DIFN-IKDEANKQTTLQKNAIDGIVHIFDMSDEQGIVHMGVPTG 115

Oy 129 FTLPGSTTVCGDSHTSTHGAFLAAGIGTSEVEHVLATOCLLIKRSKMNRQODGELAP 188
Db 116 LTQPGKTVICGDSHTATHGAFLAAGIGTSEVEHVLATOCLLQKPLNKLIDINGTLPT 175

Oy 189 QVSSKDVVLHAIGIIGTAGGTGAVIEPGSVRSLSMEARMSICNMSLEGGRAGMVPD 248
Db 176 GYVAKDILHLIKTYGVDFGTYGALETGETKJKNLSMDGRMTCNMAIEGAKYGIQPD 235

Oy 249 BTFEYVLKGRPLAKYDPSPEWKATODVKNLQSDPGKYLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 308
Db 236 DTFEYVKGRPPADNF----AKSVDKWRELYSDDDAI.FDRVIEFDVSTLEPQVWTGTPN 290

Oy 309 EDVVPITGVVVDPDPEFATEAKKADGRMLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 368
Db 291 EMGVNNSEPFP----EISDINDQRAYDNGLEPGKQAKEDDLGIVFLGSCTNARLSD 343

Oy 369 IAAAAAVVKGRKKAPVNSKAMVPGSLVYKTOAEBGLDKIFPEAGPEWRAGCSCMIGM 428
Db 344 IIEASHIVVKGNVKVHPNI-TATIYVPGSRTVVKRAEKLQGIDTITKNGAFEWREPCSCMIGM 402

Oy 429 NPDQAFQERCASTSNENFEGRQGAGGRTHLNSPVMAAAGIVGKLAQVRLKLTDYKASPH 488
Db 403 NPDQVPEGVHCASTSNENFEGRQGKGAHIVLSPAMAAAAGHGKFVDFVVKV----- 454

Oy 489 IAAQKSTVTKPHVDERINODAHEKDITADIPEDNNNGPHTNTSASVGTSGAFLPKFTILKG 548
Db 455 -----VVXMAIAKPIITYKG 469

Oy 549 IAAPEKANVDTDAIIPKQFLKTIKRTGLNHALFYEMRFNEDGTEKSDFVLNKEPYRKAS 608
Db 470 KIVPLFDNDIIDDQIITKVKHILKRIKSGFGPPAFDEWRYLPDCSDNPENPKPQYKGAS 529

Oy 609 ILVCTGANFGCSSLSSREHAPWALNDFGRSVATPSFADIFNNFSFKNGMLPPIKTDQOIE 668
Db 530 ILL-TGDNFGCSSLSSREHAWALKDGFHIIAGSFDFYMNCTKNAMLPVILEKNA-E 587

Oy 669 AIAAEARAGKIEVLDLPNQLIKNATGETCTFEVEEFRKHCLVNGLDIGLTMQMEDKIA 728
Db 588 HIAKYY----EIEVLDLPNQTV--SSPDRSFHFEIDETWKNLKLVNGLDDIAITLQYESLIE 641

Oy 729 EPE 731
Db 642 KYE 644

Query Match 41.1%; Score 1666.5; DB 22; Length 644;
Best Local Similarity 48.7%; Prd. No. 7.0e-157; Gaps 10;
Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10;

Qy 9 QTLYDKVLAHQHVVDEKLDGTVALYIDBHLVHEVTSQAPEGLRLQNLKLRPLTFTALD 68
Db 3 QTLFDKVWNRHVLYKGIGEPLQLYIDHLHLEVTSQAPEGLRLQNLKLRPLTFTALD 62

Qy 69 HNPVPTSRKALKDIASTPIKEDDSRTOCVTLEENVKERGTVYFGLSDKROQGIYHVGPEQ 128
Db 63 HNPVPTI----DIFN-IKDEANKQTTLQKNAIDGIVHIFDMSDEQGIVHMGVPTG 115

Qy 129 FTLPGCTVYCGDSHTSTHGAFLAAGIGTSEVEHVLATOCLLIKRSKMNRQODGELAP 188
Db 176 GYVAKDILHLIKTYGVDFGTYGALETGETKJKNLSMDGRMTCNMAIEGAKYGIQPD 235

Qy 249 BTFEYVLKGRPLAKYDPSPEWKATODVKNLQSDPGKYLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 308
Db 236 DTFEYVKGRPPADNF----AKSVDKWRELYSDDDAI.FDRVIEFDVSTLEPQVWTGTPN 290

Qy 309 EDVVPITGVVVDPDPEFATEAKKADGRMLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 368
Db 291 EMGVNNSEPFP----EISDINDQRAYDNGLEPGKQAKEDDLGIVFLGSCTNARLSD 343

Qy 369 IAAAAAVVKGRKKAPVNSKAMVPGSLVYKTOAEBGLDKIFPEAGPEWRAGCSCMIGM 428
Db 344 IIEASHIVVKGNVKVHPNI-TATIYVPGSRTVVKRAEKLQGIDTITKNGAFEWREPCSCMIGM 402

Qy 429 NPDQAFQERCASTSNENFEGRQGAGGRTHLNSPVMAAAGIVGKLAQVRLKLTDYKASPH 488
Db 403 NPDQVPEGVHCASTSNENFEGRQGKGAHIVLSPAMAAAAGHGKFVDFVVKV----- 454

Qy 489 IAAQKSTVTKPHVDERINODAHEKDITADIPEDNNNGPHTNTSASVGTSGAFLPKFTILKG 548
Db 455 -----VVXMAIAKPIITYKG 469

Qy 549 IAAPEKANVDTDAIIPKQFLKTIKRTGLNHALFYEMRFNEDGTEKSDFVLNKEPYRKAS 608
Db 470 KIVPLFDNDIIDDQIITKVKHILKRIKSGFGPPAFDEWRYLPDCSDNPENPKPQYKGAS 529

Qy 609 ILVCTGANFGCSSLSSREHAPWALNDFGRSVATPSFADIFNNFSFKNGMLPPIKTDQOIE 668
Db 530 ILL-TGDNFGCSSLSSREHAWALKDGFHIIAGSFDFYMNCTKNAMLPVILEKNA-E 587

Qy 669 AIAAEARAGKIEVLDLPNQLIKNATGETCTFEVEEFRKHCLVNGLDIGLTMQMEDKIA 728
Db 588 HIAKYY----EIEVLDLPNQTV--SSPDRSFHFEIDETWKNLKLVNGLDDIAITLQYESLIE 641

Qy 729 EPE 731
Db 642 KYE 644

Query Match 41.1%; Score 1666.5; DB 22; Length 644;
Best Local Similarity 48.7%; Prd. No. 7.0e-157; Gaps 10;
Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10;

Qy 9 QTLYDKVLAHQHVVDEKLDGTVALYIDBHLVHEVTSQAPEGLRLQNLKLRPLTFTALD 68
Db 3 QTLFDKVWNRHVLYKGIGEPLQLYIDHLHLEVTSQAPEGLRLQNLKLRPLTFTALD 62

Qy 69 HNPVPTSRKALKDIASTPIKEDDSRTOCVTLEENVKERGTVYFGLSDKROQGIYHVGPEQ 128
Db 63 HNPVPTI----DIFN-IKDEANKQTTLQKNAIDGIVHIFDMSDEQGIVHMGVPTG 115

Qy 129 FTLPGCTVYCGDSHTSTHGAFLAAGIGTSEVEHVLATOCLLIKRSKMNRQODGELAP 188
Db 176 GYVAKDILHLIKTYGVDFGTYGALETGETKJKNLSMDGRMTCNMAIEGAKYGIQPD 235

Qy 249 BTFEYVLKGRPLAKYDPSPEWKATODVKNLQSDPGKYLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 308
Db 236 DTFEYVKGRPPADNF----AKSVDKWRELYSDDDAI.FDRVIEFDVSTLEPQVWTGTPN 290

Qy 309 EDVVPITGVVVDPDPEFATEAKKADGRMLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 368
Db 291 EMGVNNSEPFP----EISDINDQRAYDNGLEPGKQAKEDDLGIVFLGSCTNARLSD 343

Qy 369 IAAAAAVVKGRKKAPVNSKAMVPGSLVYKTOAEBGLDKIFPEAGPEWRAGCSCMIGM 428
Db 344 IIEASHIVVKGNVKVHPNI-TATIYVPGSRTVVKRAEKLQGIDTITKNGAFEWREPCSCMIGM 402

Qy 429 NPDQAFQERCASTSNENFEGRQGAGGRTHLNSPVMAAAGIVGKLAQVRLKLTDYKASPH 488
Db 403 NPDQVPEGVHCASTSNENFEGRQGKGAHIVLSPAMAAAAGHGKFVDFVVKV----- 454

Qy 489 IAAQKSTVTKPHVDERINODAHEKDITADIPEDNNNGPHTNTSASVGTSGAFLPKFTILKG 548
Db 455 -----VVXMAIAKPIITYKG 469

Qy 549 IAAPEKANVDTDAIIPKQFLKTIKRTGLNHALFYEMRFNEDGTEKSDFVLNKEPYRKAS 608
Db 470 KIVPLFDNDIIDDQIITKVKHILKRIKSGFGPPAFDEWRYLPDCSDNPENPKPQYKGAS 529

Qy 609 ILVCTGANFGCSSLSSREHAPWALNDFGRSVATPSFADIFNNFSFKNGMLPPIKTDQOIE 668
Db 530 ILL-TGDNFGCSSLSSREHAWALKDGFHIIAGSFDFYMNCTKNAMLPVILEKNA-E 587

Qy 669 AIAAEARAGKIEVLDLPNQLIKNATGETCTFEVEEFRKHCLVNGLDIGLTMQMEDKIA 728
Db 588 HIAKYY----EIEVLDLPNQTV--SSPDRSFHFEIDETWKNLKLVNGLDDIAITLQYESLIE 641

Qy 729 EPE 731
Db 642 KYE 644

Query Match 41.1%; Score 1666.5; DB 22; Length 644;
Best Local Similarity 48.7%; Prd. No. 7.0e-157; Gaps 10;
Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10;

Qy 9 QTLYDKVLAHQHVVDEKLDGTVALYIDBHLVHEVTSQAPEGLRLQNLKLRPLTFTALD 68
Db 3 QTLFDKVWNRHVLYKGIGEPLQLYIDHLHLEVTSQAPEGLRLQNLKLRPLTFTALD 62

Qy 69 HNPVPTSRKALKDIASTPIKEDDSRTOCVTLEENVKERGTVYFGLSDKROQGIYHVGPEQ 128
Db 63 HNPVPTI----DIFN-IKDEANKQTTLQKNAIDGIVHIFDMSDEQGIVHMGVPTG 115

Qy 129 FTLPGCTVYCGDSHTSTHGAFLAAGIGTSEVEHVLATOCLLIKRSKMNRQODGELAP 188
Db 176 GYVAKDILHLIKTYGVDFGTYGALETGETKJKNLSMDGRMTCNMAIEGAKYGIQPD 235

Qy 249 BTFEYVLKGRPLAKYDPSPEWKATODVKNLQSDPGKYLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 308
Db 236 DTFEYVKGRPPADNF----AKSVDKWRELYSDDDAI.FDRVIEFDVSTLEPQVWTGTPN 290

Qy 309 EDVVPITGVVVDPDPEFATEAKKADGRMLQYMLKAGTPEMDIPVDKWFIGSCTNSRIED 368
Db 291 EMGVNNSEPFP----EISDINDQRAYDNGLEPGKQAKEDDLGIVFLGSCTNARLSD 343

Qy 369 IAAAAAVVKGRKKAPVNSKAMVPGSLVYKTOAEBGLDKIFPEAGPEWRAGCSCMIGM 428
Db 344 IIEASHIVVKGNVKVHPNI-TATIYVPGSRTVVKRAEKLQGIDTITKNGAFEWREPCSCMIGM 402

Qy 429 NPDQAFQERCASTSNENFEGRQGAGGRTHLNSPVMAAAGIVGKLAQVRLKLTDYKASPH 488
Db 403 NPDQVPEGVHCASTSNENFEGRQGKGAHIVLSPAMAAAAGHGKFVDFVVKV----- 454

Qy 489 IAAQKSTVTKPHVDERINODAHEKDITADIPEDNNNGPHTNTSASVGTSGAFLPKFTILKG 548
Db 455 -----VVXMAIAKPIITYKG 469

Qy 549 IAAPEKANVDTDAIIPKQFLKTIKRTGLNHALFYEMRFNEDGTEKSDFVLNKEPYRKAS 608
Db 470 KIVPLFDNDIIDDQIITKVKHILKRIKSGFGPPAFDEWRYLPDCSDNPENPKPQYKGAS 529

QY 609 ILVCTGANFGCSSREHAPEWALNDFGTIPRVSIAFPNSPKNGMLPIPKDQAOIE 668
 Db 530 ILI-TGDNFGCGSSREHAWALKDYGFHIIAGSFSDIFYMCTKNAULPIVLEKNAR-E 587
 QY 669 AIAEARGKEIEVDLNPQNTV-SSPDKFHFEIDETWKNLVNGLDDIAITQYESLIE 641
 QY 729 EFE 731
 Db 642 KYE 644

RESULT 24
 US-10-072-851-5730
 ; Sequence 5730, Application US/10072851
 ; GENERAL INFORMATION:
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Xu, H. Howard
 ; APPLICANT: Foulkes, J. Gordon
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Hasselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Roemer, Terry
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Boone, Charles
 ; APPLICANT: Bussey, Howard
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
 ; FILE REFERENCE: ELITRA.028A
 ; CURRENT APPLICATION NUMBER: US/10/072,851
 ; CURRENT PILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 15811
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5730
 ; LENGTH: 644
 ; TYPE: PRT
 ; ORGANISM: *Staphylococcus aureus*
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)..(644)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-10-072-851-5730

Query Match 41.1%; Score 1666.5; DB 24; Length 644;
 Best Local Similarity 48.7%; Pred. No. 7.8e-157; Mismatches 198; Indels 81; Gaps 10;
 Matches 352; Conservative 92; N mismatches 198; Indels 81; Gaps 10;

QY 9 OTLYDKVLOAQHVDKEDLGTVLVLIDRHLVHEVTSPOFEGLNRAGKVRPDTLTTD 68
 Db 3 QTLFDKVNWRHVLYGKLGEPQOLYIDHLHIEVTSPOQAFEGLRLQRKLRPDTLTTD 62

QY 6 9 HNPVPTTSRKALKDIASFIKEDSRTOCVTLEENVKERFGVYFGSDKRGQIVWIGPQQG 128
 Db 6 3 HNVPTT-----DIFN-IKDEIAKQIITLQKNAIDFGVHIFMGSDQGIVWVGPTG 115

QY 129 FTLPGTIVVCGDSHTSTGAGFAGLAFGGTSEVERHVLATCQTLKRSKMRQYDGEIAP 188
 Db 116 LTQPGKTVICGDSHTATGAGFAGLAFGGTSEVERHVLATCQTLKRSKMRQYDGEIAP 175

QY 189 GVSSKDVWTHAIGIIIGTAGGTGAVIEFGVSVRSLSMARMSTCNMSIEGARAGMVAAP 248
 Db 176 GYVAKDILHLIKTYGVDFGTFGTYALEFGETIKNLMSDGRMTINMAIEGKARYGIIQED 235

QY 249 EITFEVKGRLPLAKVPSPEWHIKATQWKNLQSDPGAXXIDVFDADKIVPILTWGSP 308

RESULT 24
 US-10-072-851-5730
 ; Sequence 5730, Application US/10072851
 ; GENERAL INFORMATION:
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Xu, H. Howard
 ; APPLICANT: Foulkes, J. Gordon
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Hasselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Roemer, Terry
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Boone, Charles
 ; APPLICANT: Bussey, Howard
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
 ; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
 ; FILE REFERENCE: ELITRA.028A
 ; CURRENT APPLICATION NUMBER: US/10/072,851
 ; CURRENT PILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 15811
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5730
 ; LENGTH: 644
 ; TYPE: PRT
 ; ORGANISM: *Staphylococcus aureus*
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)..(644)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-10-072-851-5730

Query Match 41.1%; Score 1666.5; DB 24; Length 644;
 Best Local Similarity 48.7%; Pred. No. 7.8e-157; Mismatches 198; Indels 81; Gaps 10;
 Matches 352; Conservative 92; N mismatches 198; Indels 81; Gaps 10;

QY 9 OTLYDKVLOAQHVDKEDLGTVLVLIDRHLVHEVTSPOFEGLNRAGKVRPDTLTTD 68
 Db 3 QTLFDKVNWRHVLYGKLGEPQOLYIDHLHIEVTSPOQAFEGLRLQRKLRPDTLTTD 62

QY 9 OTLYDKVLOAQHVDKEDLGTVLVLIDRHLVHEVTSPOFEGLNRAGKVRPDTLTTD 68
 Db 3 QTLFDKVNWRHVLYGKLGEPQOLYIDHLHIEVTSPOQAFEGLRLQRKLRPDTLTTD 62

Db 116 LTQPGKTTIVCCDSHTATHGAAFGAIAFGIGTSEVERVHATQTIWQTKPKNLKLDINGTLPT 175
 Qy 189 GVSSKDVVLHIGITGTTAGGGAVIEFCGSTRSLEMAEISCNSTEGGARAGMVAPD 248
 Db 176 GYAKDILHHLIKTYGVDFGTYALBETGETIKNLNSDGRMITCNNAIEGGAKYGIQPD 235
 Qy 249 EITPEYLKGRPLAPKXDSPEWKAHQTYQWKNLQSDPQAKYDIDVFDIAKDYPTLWGTSP 308
 :
 Db 236 DITPEYVKGRPFADNF----AKSVDKWRELYSDDAIFDRYIELDVSTLEFQVTTGCTNP 290
 Qy 309 EDVVPATGVVDPETPATEAKKADGERMLQWGLKAGTPMEDIPIVDKVFIGCTNSRIED 368
 :
 Db 291 EMGVNFSEPFB----EISDINDQRAYDINGLEPCQKAEDIDLGYVFLGSCTNARLSD 343
 Qy 369 I.RAAAAYVKGRKKAAPVYKSAVNPVGSLVVKTOAEERGLDKFEAEAGFEWRAGCSMCLGM 428
 :
 Db 344 IIEASHITVKGRVKHPN----TAIVPGSSTVKREAEKGUDTIFKNAGFEWRPGCSMCLGM 402
 Qy 429 NPDLAPQERCCASTSNRNFEGRQAGGRTHLSPVNAAAAGIVGKLADEVRKLTDYKASPH 488
 :
 Db 403 NPDQVPEGVHCAOSTSNRNFEGRQGKARTHLYSPVNAAAATHGKFYDVVKY----- 454
 Qy 489 IAAQKSTVTPHVDERINQDAHEKDIADFEPDNNGPHNTSASVGTSGALPKFTILKG 548
 :
 Db 455 -----VYXMAALKPITTYKG 469
 Qy 549 IAAPELKANVDTDAIIPQKFUTKIKRTGLGNALFYENRFNEDOTEKEDFVLAKEPYKAS 608
 :
 Db 470 KIVPLFNDNIDDQIIPKVLHKLRIKSGFGPPADEFWRYLPDOSDNDFNPNKPOYKGAS 529
 Qy 609 I.LVCTGANFGGSSREHAPWALNDFGIRSVLAPSFDJIFFNNSFKNGMLPPIKDOAQIE 668
 :
 Db 530 I.II-TGDNFGCCSSREHAAWALKDYGHIIITAGSFSDIYMNCTKNMLPYLEKNR-E 587
 Qy 669 AIAAEARAGKEI.EVDPNQLKNAUTGETICTEVEEPRKHCLVNGLDDIGLTMQMEDKIA 728
 :
 Db 588 HLAKEYV----ETEVDLPLNQTV--SSPDKSFHEDETWKNLVNGLDDIAITLQYESLIE 641
 Qy 729 EPE 731
 :
 Db 642 RYE 644

Search completed: March 17, 2003, 08:53:54
 Job time : 169 secs